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NASA TM X-52471

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MODEL SAMPLING APPLIED TO THE NORMAL SHOCK PROBLEM

by Morris Perlmutter
Lewis Research Center
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TECHNICAL PAPER proposed for presentation at Sixth International Symposium on Rarefied Gas Dynamics Cambridge, Massachusetts, July 22-26, 1968

NATIONAL AERONAUTICS AND SPACE ADMINISTRATION · WASHINGTON, D.C. · 1968

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ABSTRACT

Model sampling or monte carlo is applied to the normal shock problem. Temperature and density profiles through the shock for Mach number of 10 are given. It was assumed that the intermolecular collisions were Maxwellian and that the target molecules had a two sided half maxwellian distribution. The results show a significant difference from previous analytical solutions. Importance sampling is used to reduce the solution variance.

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Model sampling analysis has been used previously in rarefied gas problems (refs. 1 and 2). This approach is extended to the solution of the normal shock problem at high Mach numbers for which at the present time no exact solution exists. The analytical model is shown in Fig. 1. The average quantity Q per molecule transported across the scoring cross section p can be obtained by scoring the weights times the quantity Q of the sample molecules passing that cross section.

$$\frac{\left(\sum^{s_+} WQ - \sum^{s_-} WQ\right)_p}{\left(\sum^{s_+} W - \sum^{s_-} W\right)_p} \approx \frac{\left[\rho \int (WQ)\left(\frac{v_1 f}{W}\right) dv\right]_p}{\left[\rho \int W \left(\frac{v_1 f}{W}\right) dv\right]_p} \qquad (1)$$

where f is the local velocity distribution at point p, s_+ is the number of sample molecules passing p in the positive v_1 direction and W is the weight of the sample molecule. The local distribution from which the sampling is done, $(v_1 f/W)_p$, is obtained by following probable his-

tories of sample molecules of weight W from their known initial positions to the scoring position. If the weight of the entering upstream molecule, W_0, is taken as $\bar{v}_1$ then the average Q at position p can be found to be

$$(\rho\langle Q\bar{v}_1\rangle)_p \approx \frac{\rho_{+0}}{s_{+0}}\left(\sum^{s_+} WQ - \sum^{s_-} WQ\right)_p \qquad (2)$$

where

$$\rho_{+0} = \rho_{fo} \int_{\bar{v}_1>0,x=0} f_M \, d^3\bar{v}$$

f_M being the maxwellian distribution. The weight of the entering upstream sample molecule was chosen so as to minimize the variance of the density at the upstream scoring position. Thus from (Eq. (2)) we can find the local density from

$$\rho = \rho_+ + \rho_- = \frac{\rho_{+0}}{s_{+0}}\left(\sum^{s_+} \frac{W}{\bar{v}_1} - \sum^{s_-} \frac{W}{\bar{v}_1}\right)_p \qquad (3)$$

Similarly the other local flow characteristics can be found.

The sample histories originate upstream and downstream from the shock. The velocity of the sample molecule entering the first zone upstream from the shock is picked from

$$\left(\frac{\bar{v}_1 f_M}{W}\right)_{o,\bar{v}_1>0} = (f_M)_{o,\bar{v}_1>0}$$

After the sample molecule enters the zone we must determine the path length to collision. The distribution of path lengths to collision is given by $\exp(-\delta/\lambda_p)/\lambda_p$ where the mean free path λ_p is given by $(K_n)_p(\bar{v}_s/\rho)$. The δ picked is compared to the distance across the zone, $1/p_f$, to determine if a collision has occured. To determine the distance across the zones we use

$$\frac{x_p}{\lambda_{\mu,0}} = \frac{15\sqrt{\pi}}{p_f 16} \frac{A_2(5)}{(v_0)^2_{max}} \left(\sum_1^p \frac{1}{K_n} \right) \qquad (4)$$

If a collision has occured we pick a target molecule collision partner from the distribution of target molecules which was assumed to be a two sided maxwellian as in Ref. 1. The parameters of the target molecule distribution are obtained from the sample molecule scoring results and the problem iterated. The sample molecule and target molecule are assumed to have maxwellian collisions.

Results

The resulting profiles for upstream Mach number of 10 are shown in Fig. 2. The present results are compared to the bimodel model (Ref. 3) and the Navier Stokes results given in Ref. 4. The density curve fall along the bimodel results upstream of the shock and close to the N.S. downstream while the temperature curve fall above the bimodel and N.S. results upstream and close to the bimodel through the rest of the shock.

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MODEL FOR NORMAL SHOCK

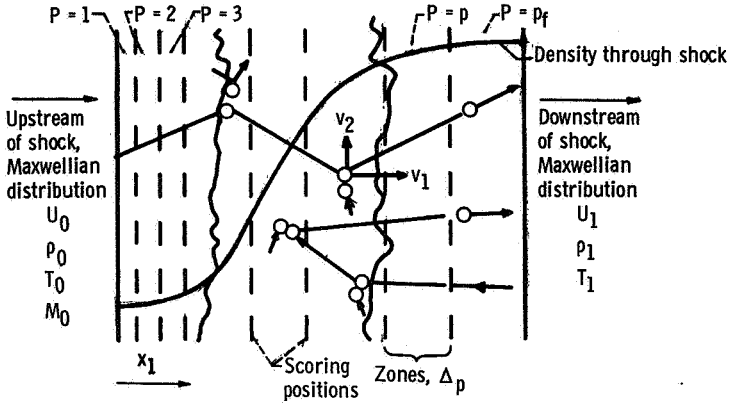

Fig. 1. - Model for normal shock.

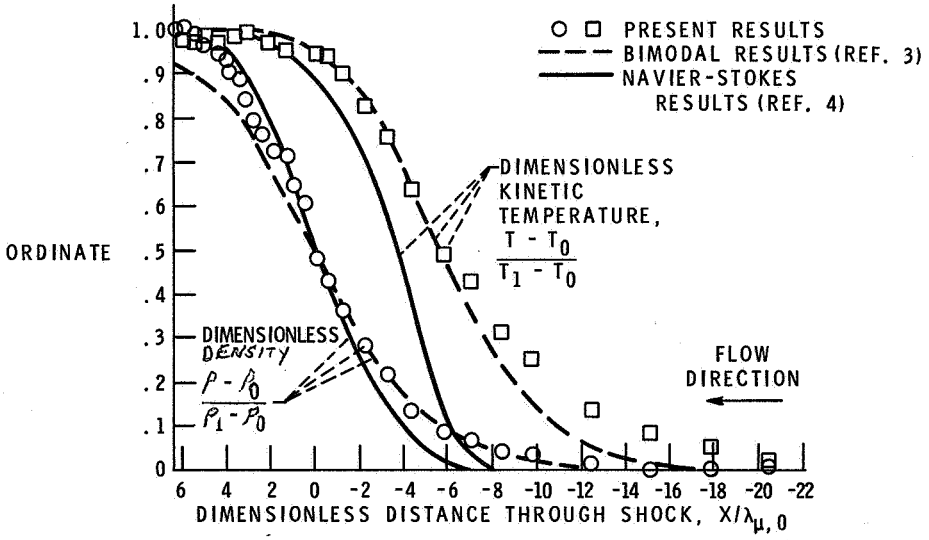

Fig. 2. - Density and temperature profiles through shock. Mach 10, two sided Maxwellian target molecule distribution, Maxwellian intermolecular collisions.